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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,168

DATE: 12/31/2001
TIME: 12:49:21

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\12312001\J017168.raw

ENTERED

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3 <110> APPLICANT: The United States of America as Represented by the Secretary of the
4     Department of Health and Human Services, Centers for Disease Control and
5     Prevention
6     Liu, Hsi
7     Steiner, Bret
8     Berta, Rodas
10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING TREPONEMA PALLIDUM
12 <130> FILE REFERENCE: 6395-61666
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/017,168
C--> 14 <141> CURRENT FILING DATE: 2001-12-14
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/16425
15 <151> PRIOR FILING DATE: 2000-06-14
17 <150> PRIOR APPLICATION NUMBER: US 60/138,981
18 <151> PRIOR FILING DATE: 1999-06-14
20 <160> NUMBER OF SEQ ID NOS: 26
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2945
26 <212> TYPE: DNA
27 <213> ORGANISM: Treponema pallidum
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (919)..(2217)
32 <223> OTHER INFORMATION:
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <223> OTHER INFORMATION: Subspecies: pallidum (Nichols strain)
40 <400> SEQUENCE: 1
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45 tccccatctt ccgatactgg atcgggtgctg gggggagtag gagtggggaa gcgtctgtgc      180
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49 tacgtgcccg ttcacgcag tgggggctct caagattcga gcatgagcac agcagtgggc      300
51 gatacgctcc ttaacgcctt cttcgacgag ggaatggtgg ttacggcagt accgccgggt      360
53 gtacacgacg gccagactat agcagaaaatt gctgcatgtt ttgaagtaat gcccgattac      420
55 gcgtgtgttg tgcagtttca ttccgctcgt ctccctgggtg gggaaagccc tacctcccgt      480
57 gcccgcgcg cttggtcttc agagaggttc cgtgctgtgt ggacattagt ggatttgcatt      540
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61 gagtgtgttg acgtcgttac ccgttgtatt gcggagcagg caatttcgta catacgggtg      660
63 ggcacgagca ccgatacagc cggagttcag ttatagaaaa tagggaatac gtaaggtgtc      720
65 tgcagcgctg cttcagctgg gaggagtctt atgattaaac gccacatgtt cgcaaaaagg      780
67 ggtgtcaaag gaagatctta cctggttagg gtgaacactg cgttcttagt gctttgtgtt      840
69 gcttctgtca cgccgctttg ggctgtgtgg gaagggaatg cagaaattgg cccccagga      900
71 agttttctgc aggacggc atg ttt gtg cgc agt gac atg ttc ccc aaa aac      951
72                               Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn
73                               1                               5                               10
75 act gct gtt gaa att agc aac tta gaa aag aat gcc aag gct cag gca      999

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77          15          20          25
79 gtg gtt att ggg cac gca ggg atc ccc ggt ctt cta gtt agc ctt gca      1047
80 Val Val Ile Gly His Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala
81          30          35          40
83 ccc gct gct gca gca cag ctt ggg att ggc gta tac caa gct gtg cgt      1095
84 Pro Ala Ala Ala Ala Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg
85          45          50          55
87 gta cgc gta cgt acc ttg ggt acc gtg cgc ggt ggg tct caa aca agt      1143
88 Val Arg Val Arg Thr Leu Gly Thr Val Arg Gly Gly Ser Gln Thr Ser
89 60          65          70          75
91 cag gac gga ctg tcc ctt gca tct ttg ccg tcc cgt gtg cct gcg cgc      1191
92 Gln Asp Gly Leu Ser Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg
93          80          85          90
95 ccc gcg cag cgt gat cct ctg tca tcc ccg ccg gca ggt cac act gta      1239
96 Pro Ala Gln Arg Asp Pro Leu Ser Ser Pro Pro Ala Gly His Thr Val
97          95          100          105
99 ccg gaa tat cgc gat acg gtt att ttc gat gac ccg cgt ttg gtt tcc      1287
100 Pro Glu Tyr Arg Asp Thr Val Ile Phe Asp Asp Pro Arg Leu Val Ser
101          110          115          120
103 cct ttg tct cgt gag gtg gag gac gcg ccg aag gta gtg gag ccg gcc      1335
104 Pro Leu Ser Arg Glu Val Glu Asp Ala Pro Lys Val Val Glu Pro Ala
105          125          130          135
107 tct gag cgt gag gga ggg gag cgt gag gtg gag gac gcg ccg aag gta      1383
108 Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Ala Pro Lys Val
109 140          145          150          155
111 gtg gag ccg gcc tct gag cgt gag gga ggg gag cgt gag gtg gag gac      1431
112 Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Arg Glu Val Glu Asp
113          160          165          170
115 gtg ccg aag gta gtg gag ccg gcc tct gag cgt gag gga ggg gag cgt      1479
116 Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg
117          175          180          185
119 gag gtg gag gac gcg ccg aag gta gtg gag ccg gcc tct gag cgt gag      1527
120 Glu Val Glu Asp Ala Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu
121          190          195          200
123 gga ggg gag cgt gag gtg gag gac gtg ccg aag gta gtg gag ccg gcc      1575
124 Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala
125          205          210          215
127 tct gag cgt gag gga ggg gag cgt gag gtg gag aac gtg ccg aag gta      1623
128 Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asn Val Pro Lys Val
129 220          225          230          235
131 gtg gag ccg gcc tct gag cgt gag gga ggg gag cgt gag gtg gag gac      1671
132 Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp
133          240          245          250
135 gcg ccg aag gta gtg gag ccg gcc tct gag cgt gag gga ggg gag cgt      1719
136 Ala Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg
137          255          260          265
139 gag gtg gag gac gcg ccg aag gta gtg gag ccg gcc tct gag cgt gag      1767
140 Glu Val Glu Asp Ala Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu

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141          270          275          280
143 gga ggg gag cgt gag gtg gag gac gtg ccg aag gta gtg gag ccg gcc      1815
144 Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala
145          285          290          295
147 tct gag cgt gag gga ggg gag cgt gag gtg gag gac gtg ccg aag gta      1863
148 Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val
149 300          305          310          315
151 gtg gag ccg gcc tct gag cgt gag gga ggg gag cgt gag gtg gag gac      1911
152 Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp
153          320          325          330
155 gtg ccg aag gta gtg gag ccg gcc tct gag cgt gag gga ggg gag cgt      1959
156 Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg
157          335          340          345
159 gag gtg gag gac gtg ccg aag gta gtg gag ccg gcc tct gag cgt gag      2007
160 Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu
161          350          355          360
163 gga ggg gag cgt gag gtg gag gac gtg ccg ggg gta gtg gag ccg gcc      2055
164 Gly Gly Glu Arg Glu Val Glu Asp Val Pro Gly Val Val Glu Pro Ala
165          365          370          375
167 tct ggg cat gaa gga ggg gag cgt gag gtg gag gac gtg ccg ggg gta      2103
168 Ser Gly His Glu Gly Gly Glu Arg Glu Val Glu Asp Val Pro Gly Val
169 380          385          390          395
171 gtg gag ccg gcc tct ggg cat gaa gga ggg gag cgt gag gtc gct tct      2151
172 Val Glu Pro Ala Ser Gly His Glu Gly Gly Glu Arg Glu Val Ala Ser
173          400          405          410
175 cag cat acg aag cag cca tcc cac tcg gtt tcc aac tca gct ccc aat      2199
176 Gln His Thr Lys Gln Pro Ser His Ser Val Ser Asn Ser Ala Pro Asn
177          415          420          425
179 cag ttt cgg aaa ccc tga gggggaactc ccctttacgc tccctgacct      2247
180 Gln Phe Arg Lys Pro
181          430
183 atccgagtgca gaaattgtgg ttccggagga acagaaaagga cgtgcgcacgc cccaggtgat      2307
185 acccgagggt ggcgccacgtg gactgcaacc tgggtgaatac tacgtacaga ttgcagtctt      2367
187 tcatgacgct atccaggtgc agagcattgt ccaccgttac ggggtagaat accccatcgc      2427
189 agtggagcag gacatccatg aaggtaaggt gcgtttcacc gtatgcgtcg gtcctgtcca      2487
191 aaaagacgaa cgcggcgcgg tactagagaa cttccaaagg tttggattca aggacgcctt      2547
193 tctgaaaaag gcgcgatgat caggtcggcc ctctcttcc cctcgtgacc gtggtgactc      2607
195 gccccgaagg gggcgcacag agcccgaagg aacggaaggg aaggggcaga cttaactatt      2667
197 tctttgtttt tttagcacg taaaacggcg ccattctcctt tgaaggcttt cctgcgccgg      2727
199 gagcgcgccat gtagcgaacg gagttactgt ctatcagctc gtacagctct ttctcgtgcg      2787
201 gtgccttcga ttgctccgag gacacaagcg agagttcgac aattccgtct tcacgtacca      2847
203 tccacgtacc gcgatacgta agaggagaag gtgccgactt cttctcaagg gcaagctcta      2907
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208 <210> SEQ ID NO: 2
209 <211> LENGTH: 432
210 <212> TYPE: PRT
211 <213> ORGANISM: Treponema pallidum
213 <220> FEATURE:
214 <221> NAME/KEY: misc_feature

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215 <223> OTHER INFORMATION: Subspecies: pallidum (Nichols strain)
 217 <400> SEQUENCE: 2
 219 Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile
 220 1 5 10 15
 223 Ser Asn Leu Glu Lys Asn Ala Lys Ala Gln Ala Val Val Ile Gly His
 224 20 25 30
 227 Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala
 228 35 40 45
 231 Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Val Arg Thr
 232 50 55 60
 235 Leu Gly Thr Val Arg Gly Gly Ser Gln Thr Ser Gln Asp Gly Leu Ser
 236 65 70 75 80
 239 Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg Pro Ala Gln Arg Asp
 240 85 90 95
 243 Pro Leu Ser Ser Pro Pro Ala Gly His Thr Val Pro Glu Tyr Arg Asp
 244 100 105 110
 247 Thr Val Ile Phe Asp Asp Pro Arg Leu Val Ser Pro Leu Ser Arg Glu
 248 115 120 125
 251 Val Glu Asp Ala Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly
 252 130 135 140
 255 Gly Glu Arg Glu Val Glu Asp Ala Pro Lys Val Val Glu Pro Ala Ser
 256 145 150 155 160
 259 Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val
 260 165 170 175
 263 Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Ala
 264 180 185 190
 267 Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu
 268 195 200 205
 271 Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly
 272 210 215 220
 275 Gly Glu Arg Glu Val Glu Asn Val Pro Lys Val Val Glu Pro Ala Ser
 276 225 230 235 240
 279 Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Ala Pro Lys Val Val
 280 245 250 255
 283 Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Ala
 284 260 265 270
 287 Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu
 288 275 280 285
 291 Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly
 292 290 295 300
 295 Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser
 296 305 310 315 320
 299 Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val
 300 325 330 335
 303 Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val
 304 340 345 350
 307 Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu
 308 355 360 365
 311 Val Glu Asp Val Pro Gly Val Val Glu Pro Ala Ser Gly His Glu Gly

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312      370      375      380
315 Gly Glu Arg Glu Val Glu Asp Val Pro Gly Val Val Glu Pro Ala Ser
316 385      390      395      400
319 Gly His Glu Gly Gly Glu Arg Glu Val Ala Ser Gln His Thr Lys Gln
320      405      410      415
323 Pro Ser His Ser Val Ser Asn Ser Ala Pro Asn Gln Phe Arg Lys Pro
324      420      425      430
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 699
329 <212> TYPE: DNA
330 <213> ORGANISM: Treponema pallidum
332 <220> FEATURE:
333 <221> NAME/KEY: CDS
334 <222> LOCATION: (1)..(699)
335 <223> OTHER INFORMATION:
338 <220> FEATURE:
339 <221> NAME/KEY: misc_feature
340 <223> OTHER INFORMATION: Subspecies: pertenue (CDC-2 strain)
343 <400> SEQUENCE: 3
344 atg ttt gtg cgc agt gac atg ttc ccc aaa aac act gct gtt gaa att      48
345 Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile
346 1      5      10      15
348 agc aac tta gaa aag aat gcc aag gct cag gca gtg gtt att ggg cac      96
349 Ser Asn Leu Glu Lys Asn Ala Lys Ala Gln Ala Val Val Ile Gly His
350      20      25      30
352 gca ggg atc ccc ggt ctt cta gtt agc ctt gca ccc gct gct gca gca      144
353 Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala Ala
354      35      40      45
356 cag ctt ggg att ggc gta tac caa gct gtg cgt gta cgc gta cgt acc      192
357 Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Val Arg Thr
358      50      55      60
360 ttg ggt acc gtg cgc ggt ggg tct caa aca agt cag gac gga ctg tcc      240
361 Leu Gly Thr Val Arg Gly Gly Ser Gln Thr Ser Gln Asp Gly Leu Ser
362 65      70      75      80
364 ctt gca tct ttg ccg tcc cgt gtg cct gcg cgc ccc gcg cag cgt gat      288
365 Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg Pro Ala Gln Arg Asp
366      85      90      95
368 cct ctg tca tcc ccg ccg gca ggt cac act gta ccg gaa tat cgc gat      336
369 Pro Leu Ser Ser Pro Pro Ala Gly His Thr Val Pro Glu Tyr Arg Asp
370      100      105      110
372 acg gtt att ttc gat gac ccg cgt ttg gtt tcc cct ttg tct cgt gag      384
373 Thr Val Ile Phe Asp Asp Pro Arg Leu Val Ser Pro Leu Ser Arg Glu
374      115      120      125
376 gtg gag gac gtg ccg aag gta gtg gag ccg gcc tct gag cgt gag gga      432
377 Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly
378      130      135      140
380 ggg gag cgt gag gtg gag gac gtg ccg aag gta gtg gag ccg gcc tct      480
381 Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser
382 145      150      155      160

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VERIFICATION SUMMARY

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Input Set : A:\pto.vsk.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date